of biological systems and have been applied for protein systems with small charge polarization. However, these means are not suitable to obtain the ensemble of histone tails in a form of a nucleosome, because strong electrostatic interactions between positively charged histone tails and negatively charged DNA compared with those in regular protein systems makes difficult to realize a sufficient sampling. Thus, we applied adaptive lambda square dynamics (ALSD) simulation we developed recently to investigate the conformations of H3 histone tails. ALSD dynamically scales the simulation parameters (charge, van der Walls and torsion energies) only for the histone tails during the simulations. This successfully sampled various histone tail conformations. In this poster, we introduce the ALSD simulation results and the differences in conformational ensembles between unmodified and acetylated H3 histone tails.

2739-Pos Board B169

Dynamics of the Nucleosome Core Particle Revealed from a New Database of High-Resolution X-Ray Crystallographic and Simulated Structures

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The nucleosome core particle is a highly conserved structure which can play diverse roles depending on the organism, cell, or part of chromatin in which it resides. The Protein Data Bank currently contains approximately 90 nucleosome core particle structures, most of which were determined in the last five years. The recent emergence of the field of epigenetics, and the increase in data available from experiments, warrants a need to develop new approaches to compare features of interest across multiple structures.

The growing ensemble of structural data garnered from in vitro and in silico experiments provides a unique platform to study the mechanochemical properties of the nucleosome. We have developed a database and new computational tools to allow researchers to analyze and compare the nucleosome core particle structures deposited in the Protein Data Bank. The features of the DNA-protein assembly can be examined in novel coordinate frames placed on the structure, allowing researchers to obtain a better understanding of the organization and subtleties of the macromolecular complexes. This comparison allows one to examine the 'motion' of specific residues of interest, including specific sites of post-translational histone modification. The database also includes DNA-histone contact points, DNA conformational parameters, and information about protein features such as the secondary structure in the globular histone core and the 'motion' of the histone tails. Along with these features, we also characterize the dynamics of the global structure of the nucleosome core particle, including changes in the superhelical path of the DNA, rearrangements of the histone tetramers, and nucleosome stacking inside crystals. This information allows us to understand and model the critical role of mono-nucleosome structural propensity in processes such as carcinogenic modifications of the DNA, and nucleosome remodeling.

2740-Pos Board B170

The Effect of Nucleosome Unwrapping on Chd1-Induced Chromatin Remodeling

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The tight wrapping of DNA into nucleosomes reduces access and can provide a barrier for gene expression. Chromatin remodelers are responsible for sliding the nucleosome into a position where the DNA can be readily processed but the precise mechanism is unclear. The DNA in the nucleosome dynamically unwraps and rewraps around the histone core, which may affect how the chromatin remodeler binds to the nucleosome and facilitates sliding. Unwrapping is a natural response to proteins binding to DNA at the edge of the nucleosome, and can also be affected by DNA sequence. Chromodomain Helicase DNA Binding Protein 1 (Chd1) is an ATP-dependent chromatin remodeler that is responsible for transcription-related chromatin remodeling, generating evenly spaced nucleosomal arrays across the genome. We made unwrapping variants by perturbing DNA-histone interactions to see what effect this might have on Chd1's ability to slide nucleosomes. We find that unwrapping DNA from the histone slows Chd1-induced sliding. We are investigating the effects of proteins binding to the edge of the nucleosomes as well as sequence effects to understand how these influence Chd1 sliding and positional preference.

2741-Pos Board B171

Acetylation of Histone H3 Lysine 56 Abolishes Linker Histone Regulation of Transcription Factor Binding

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The linker histone H1 is an ubiquitous regulator of chromatin structure and dynamics. These linker histones are highly abundant in metazoan somatic cells with almost one linker histone per nucleosome, and regulate gene expression during development and within somatic cells. We used fluorescence resonance energy transfer (FRET) to detect changes to nucleosome wrapping, which is sensitive to both H1 binding and transcription factor binding within the nucleosome. H1 binding induces an increase in nucleosome wrapping and FRET, while transcription factor binding within the nucleosome decreases nucleosome wrapping and FRET. We find that H1 suppresses but does not abolish TF binding suggesting that H1 dynamically regulates nucleosomal DNA accessibility to TF binding. We then prepared nucleosomes with histone H3 acetylated at lysine 56 (H3K56ac). This modification is involved transcriptional regulation and increases DNA unwrapping. We find that this modification abolishes H1 suppression of TF binding within the nucleosome. This result suggests that H3K56ac can encode, within a nucleosome, H1 regulation of DNA accessibility and provides a mechanism by which H1 regulation of DNA accessibility is targeted through the genome.

2742-Pos Board B172

Mechanism of Nucleoid Collapse in E. coli

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All living cells must organize their DNA into dynamic three-dimensional architectures that are compatible with essential cellular processes such as transcription, translation, and DNA repair. Recently it has been shown that DNA is able to condense into a crystalline lattice in bacterial cells exposed to stressful conditions due to the action of a single gene. The protein responsible for creating these DNA 'biocrystals' is Dps (DNA-binding protein from starved cells) and it is essential in helping cells survive conditions ranging from starvation to antibiotic exposure. When present at sufficiently high concentrations, Dps drives the condensation of DNA into a biocrystal both in vitro and in vivo. We investigate the cooperative transition that allows Dps to rearrange the genome using a variety of techniques. We have developed a novel single molecule assay to probe the physical interactions between fluorescently tagged Dps and DNA. We find that Dps induced collapse is rate limited by a slow nucleation event but then proceeds extremely rapidly (< 100 ms). We also used magnetic tweezers to apply loads to DNA in the presence of Dps and determined collapse is much more concerted than previously assumed. We find that Dps binding to DNA displays the qualitative features of an Ising system and we have developed a mean field model that captures important features of the collapse. We look at nucleoid dynamics in single cells to test this model.

2743-Pos Board B173

The Bacterial Nucleoid Drives Cytoplasmic Dynamics

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Bacterial cells exhibit complex, cell-cycle-dependent subcellular organization despite the lack of membrane-bound organelles. One of the most popular proposed mechanisms for this cellular ultrastructure is physical exclusion from the dense bacterial nucleoid. To quantitatively investigate this hypothesis, we visualized and mapped the motion of fluorescently-tagged ectopic MS2-mRNA complexes in thousands of growing E. coli cells. We find that the the molecular complexes' motion strongly depends on their spatial position along the long-axis of the cell and that their dynamics are well characterized by a quantitative model that requires only two physical contributions: nucleoid exclusion and membrane confinement. Strikingly, we also find that the mobility of the molecular complexes is highest in regions of high nucleoid density, and that perturbations to nucleoid structure tend to increase cytoplasmic mobility. These results provide strong quantitative support for two modes of nucleoid action: (1) organizing the cell through physical exclusion forces and (2) as a facilitator of rapid motion throughout the cytoplasm. These results have potentially important biological implications and suggest that the nucleoid may play a much more direct role, than previously thought, in the organization and transport of subcellular components, including large protein complexes and plasmids.

2744-Pos Board B174

Acto-Myosin Contractility Regulates Nuclear and Chromatin Plasticity

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The cytoskeleton can exert forces on the nucleus and chromatin via direct physical links on the nuclear envelope. Such forces provide prestress on the nucleus thereby governing its morphology. However, the role of these forces in modulating nucleus and chromatin plasticity has not yet been explored. In this project, we used micro-contact printing of fibronectin to create different substrate geometries for culturing NIH3T3 cells so as to obtain specific cytoskeletal organization and then measured the nuclear and chromatin dynamics in these cells. We observed that nuclei of cells on constrained isotropic geometry (small circle) were much more plastic than those on elongated anisotropic geometry